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SEQUENCE LISTING

<110> US ONLY:
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 5
 OTHER COUNTRIES:
 Agriculture Victoria Services Pty Ltd AND Pig Research and Development
 Corporation AND Pfizer Products Inc.

10 <120> Novel therapeutic compositions for treating infection by *Lawsonia spp.*
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 <150> US 60/249596
 <151> 2000-11-17
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 Lys Ala Leu Thr Thr Ala Ala Gly Met Leu Gly Leu Ala Ile Tyr Ser
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 45 ggc gta atg gga cgt cat ttt gaa aca att ttc tac tat att ttt aca 192
 Gly Val Met Gly Arg His Phe Glu Thr Ile Phe Tyr Tyr Ile Phe Thr

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FOOTNOTES - 110904

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25 85 90 95

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45 165 170 175

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25 gat gta aga gtt att gca gca aca aat aag aat ctt gaa gac gct att 864
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 85 90 95

20 ata tta tta gct tca gca cca tta cca gcg att caa gct ata aac tca 336
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 100 105 110

aat ggc aac ctt att cgt tta gat aca ctc ccc att act cat caa tct 384
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Glu Leu Val Ile Ile Ile Gly Ala Ala Leu Gly Ala Phe Phe Ala Ser
35 40 45

Gln Thr Lys Tyr Ser Phe Thr Leu Val Ile Lys Asn Leu Ser His Ile
25 50 55 60

Phe Gly Asp Pro Asn Ser Thr Lys Ile Lys Tyr Leu Glu Thr Leu Ala
65 70 75 80

30 Leu Leu Tyr Gly Leu Phe Leu Lys Met Asn Arg Glu Gly Val Ile Ser
 85 90 95

Ile Glu Ser Asp Ile Glu Lys Pro Glu Ser Ser Pro Ile Phe Ser Lys
100 105 110

35 Tyr Pro Thr Ile Val Lys Asp Thr Lys Val Val Ala Phe Ile Ala Asp
115 120 125

Thr Leu Arg Val Tyr Leu Thr Thr Gly Ala Pro Glu Asp Ile Asp Asn
40 130 135 140

Leu Met Glu Ser Asp Met Lys Ile Thr His Glu Glu Glu Leu Leu Pro
145 150 155 160

45 Ala His Ser Ile Ser His Met Ala Glu Ser Leu Pro Gly Met Gly Ile
 165 170 175

- 16 -

Val Ala Ala Val Leu Gly Val Val Ile Thr Met Gly Lys Ile Asn Glu
 180 185 190

5 Pro Pro Glu Val Leu Gly His Tyr Ile Gly Ala Ala Leu Val Gly Thr
 195 200 205

Phe Ile Gly Ile Leu Phe Cys Tyr Gly Phe Phe Gly Pro Met Gly Ser
 210 215 220

10 Lys Leu Glu Thr Ser Ala Glu Glu Ala His Phe Tyr Tyr Asn Ser Ile
 225 230 235 240

Lys Glu Ala Val Ala Ala Ala Ile Arg Gly Ser Thr Pro Met Ile Ala
 15 245 250 255

Val Glu Tyr Gly Arg Arg Ala Ile Pro Asn Thr Phe Arg Pro Ser Phe
 260 265 270

20 Ser Glu Met Glu Glu Arg Leu Lys Thr Gly
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30 <220>
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atg gct ttc ttt cta ctg atg tgg att ctt gca atg aca ccc cct gag 96
 Met Ala Phe Phe Leu Leu Met Trp Ile Leu Ala Met Thr Pro Pro Glu
 40 20 25 30

gtt aaa gaa ggt ctt gct gca tat ttt tct tca tct gat gct aca ttt 144
 Val Lys Glu Gly Leu Ala Ala Tyr Phe Ser Ser Ser Asp Ala Thr Phe
 35 40 45

45 aaa aca cct gat agt tcg cca atc tct aac aat cct ctt atc aac caa 192

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- 17 -

	Lys	Thr	Pro	Asp	Ser	Ser	Pro	Ile	Ser	Asn	Asn	Pro	Leu	Ile	Asn	Gln	
	50						55					60					
5	ata	gat	aaa	ctt	gat	act	cga	caa	tta	aaa	att	aat	gaa	aca	gaa	caa	240
	Ile	Asp	Lys	Leu	Asp	Thr	Arg	Gln	Leu	Lys	Ile	Asn	Glu	Thr	Glu	Gln	
	65					70				75					80		
10	tct	cat	tat	gct	ctt	gct	aat	aaa	tta	aaa	aaa	atg	tta	atg	gct	gat	288
	Ser	His	Tyr	Ala	Leu	Ala	Asn	Lys	Leu	Lys	Lys	Met	Leu	Met	Ala	Asp	
				85					90				95				
15	gct	atc	cca	cag	tca	gca	aca	gga	ata	agt	gct	gac	gat	gtt	ggt	gta	336
	Ala	Ile	Pro	Gln	Ser	Ala	Thr	Gly	Ile	Ser	Ala	Asp	Asp	Val	Gly	Val	
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20	tta	tta	cgt	gta	aat	tct	aat	tcc	acg	ttt	ttt	cct	ggt	aca	gca	act	384
	Leu	Leu	Arg	Val	Asn	Ser	Asn	Ser	Thr	Phe	Phe	Pro	Gly	Thr	Ala	Thr	
				115				120					125				
25	ctt	aca	ccc	gaa	ggg	aaa	aaa	gtt	atg	gga	act	gtt	tta	gcc	gtt	ctc	432
	Leu	Thr	Pro	Glu	Gly	Lys	Lys	Val	Met	Gly	Thr	Val	Leu	Ala	Val	Leu	
				130				135					140				
30	cgt	gaa	tat	aat	ctt	tac	ctt	gtg	ata	cgt	ggc	cat	gct	gat	att	ggt	480
	Arg	Glu	Tyr	Asn	Leu	Tyr	Leu	Val	Ile	Arg	Gly	His	Ala	Asp	Ile	Gly	
				145				150					155			160	
35	gaa	ata	aca	aaa	ggc	agc	cct	ttt	gct	tct	aac	tggt	gaa	ctt	tca	gga	528
	Glu	Ile	Thr	Lys	Gly	Ser	Pro	Phe	Ala	Ser	Asn	Trp	Glu	Leu	Ser	Gly	
				165				170					175				
40	gct	cgt	gca	gct	gca	gct	gca	cag	tat	ctt	gta	gag	cac	ggg	ata	aag	576
	Ala	Arg	Ala	Ala	Ala	Ala	Ala	Gln	Tyr	Leu	Val	Glu	His	Gly	Ile	Lys	
				180				185					190				
45	gct	tca	cga	att	cgc	tct	gta	gga	tat	gca	gat	aca	aga	cct	cta	gaa	624
	Ala	Ser	Arg	Ile	Arg	Ser	Val	Gly	Tyr	Ala	Asp	Thr	Arg	Pro	Leu	Glu	
				195				200					205				
50	cct	agt	tct	cct	gaa	gga	agt	aca	aaa	aat	cgt	cgt	ata	gaa	ttc	tat	672
	Pro	Ser	Ser	Pro	Glu	Gly	Ser	Thr	Lys	Asn	Arg	Arg	Ile	Glu	Phe	Tyr	
				210				215					220				
55	ttt	cat	cgg	cca	gaa	gtt	atg	tct	tat	ggc	gtt	gta	tat	taa	tag		717
	Phe	His	Arg	Pro	Glu	Val	Met	Ser	Tyr	Gly	Val	Val	Tyr				
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 5 <212> PRT
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 15 Val Lys Glu Gly Leu Ala Ala Tyr Phe Ser Ser Ser Asp Ala Thr Phe
 35 40 45

 Lys Thr Pro Asp Ser Ser Pro Ile Ser Asn Asn Pro Leu Ile Asn Gln
 50 55 60
 20 Ile Asp Lys Leu Asp Thr Arg Gln Leu Lys Ile Asn Glu Thr Glu Gln
 65 70 75 80

 Ser His Tyr Ala Leu Ala Asn Lys Leu Lys Lys Met Leu Met Ala Asp
 25 85 90 95

 Ala Ile Pro Gln Ser Ala Thr Gly Ile Ser Ala Asp Asp Val Gly Val
 100 105 110

 30 Leu Leu Arg Val Asn Ser Asn Ser Thr Phe Phe Pro Gly Thr Ala Thr
 115 120 125

 Leu Thr Pro Glu Gly Lys Lys Val Met Gly Thr Val Leu Ala Val Leu
 130 135 140
 35 Arg Glu Tyr Asn Leu Tyr Leu Val Ile Arg Gly His Ala Asp Ile Gly
 145 150 155 160

 Glu Ile Thr Lys Gly Ser Pro Phe Ala Ser Asn Trp Glu Leu Ser Gly
 40 165 170 175

 Ala Arg Ala Ala Ala Ala Ala Gln Tyr Leu Val Glu His Gly Ile Lys
 180 185 190

 45 Ala Ser Arg Ile Arg Ser Val Gly Tyr Ala Asp Thr Arg Pro Leu Glu
 195 200 205

Pro Ser Ser Pro Glu Gly Ser Thr Lys Asn Arg Arg Ile Glu Phe Tyr
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5 Phe His Arg Pro Glu Val Met Ser Tyr Gly Val Val Tyr
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1 5 10 15

tta tgc tca atg atg gaa gct gct ata tac tct atc cct att act tat 96
 Leu Cys Ser Met Met Glu Ala Ala Ile Tyr Ser Ile Pro Ile Thr Tyr
 25 20 25 30

att gaa cac ctt cgt gaa cag gga agc aaa aaa gga gaa aaa ctt tat 144
Ile Glu His Leu Arg Glu Gln Gly Ser Lys Lys Gly Glu Lys Leu Tyr
35 40 45

tat tta cat agt aat att gat cag cct att aca gcc gta tta ata ttg 192
Tyr Leu His Ser Asn Ile Asp Gln Pro Ile Thr Ala Val Leu Ile Leu
50 55 60

35 aat act ata gca aat act gct gga gct gcc ctt gct gga gca att gct 240
 Asn Thr Ile Ala Asn Thr Ala Gly Ala Ala Leu Ala Gly Ala Ile Ala
 65 70 75 80

aca aca aca ctt cat gaa tct act aag cct ttc ttt gca gca atc ctc 288
40 Thr Thr Thr Leu His Glu Ser Thr Lys Pro Phe Phe Ala Ala Ile Leu
85 90 95

acc ttg ctt att tta gct ttt ggg gaa att ata cct aaa aca cta ggt 336
Thr Leu Leu Ile Leu Ala Phe Gly Glu Ile Ile Pro Lys Thr Leu Gly
45 100 105 110

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gtt gct tac tct aaa cgt att gct ata att ctc ctt aat cct ctc tct 384
Val Ala Tyr Ser Lys Arg Ile Ala Ile Ile Leu Leu Asn Pro Leu Ser
115 120 125

5 att ctt ata gtt act tta aaa ccc ctt att atg ctt tca agc tac tta 432
Ile Leu Ile Val Thr Leu Lys Pro Leu Ile Met Leu Ser Ser Tyr Leu
130 135 140

10 aca cga ctt gtt tca cct cga aaa cgt cct aca gtt aca gaa gat gac 480
Thr Arg Leu Val Ser Pro Arg Lys Arg Pro Thr Val Thr Glu Asp Asp
145 150 155 160

15 atc cgt gca ctt aca agt ctt tcc aga gag tct ggt cgt att aag cca 528
Ile Arg Ala Leu Thr Ser Leu Ser Arg Glu Ser Gly Arg Ile Lys Pro
165 170 175

20 tat gaa gaa cat gtc ata aaa aat atc ctt agt ctt gat tta aaa tat 576
Tyr Glu Glu His Val Ile Lys Asn Ile Leu Ser Leu Asp Leu Lys Tyr
180 185 190

gct cat gaa att atg act ccc aga act atg gtc ttt tca ctt cat gaa 624
Ala His Glu Ile Met Thr Pro Arg Thr Met Val Phe Ser Leu His Glu
195 200 205

25 aac ctt act gtc tct gaa gct tat agc aac ccc aaa ata tgg aac tat 672
Asn Leu Thr Val Ser Glu Ala Tyr Ser Asn Pro Lys Ile Trp Asn Tyr
210 215 220

30 agt cgc atc cct act tat gga gaa aat aac gaa gac att act ggc att 720
Ser Arg Ile Pro Thr Tyr Gly Glu Asn Asn Glu Asp Ile Thr Gly Ile
225 230 235 240

35 atc caa cga tat gaa att gga cga tat atg acc aat gga gaa aca gaa 768
Ile Gln Arg Tyr Glu Ile Gly Arg Tyr Met Thr Asn Gly Glu Thr Glu
245 250 255

40 aaa aaa ctt tta gaa att atg caa cca gca aaa ttt gtc ctt gaa agt 816
Lys Lys Leu Leu Glu Ile Met Gln Pro Ala Lys Phe Val Leu Glu Ser
260 265 270

'caa act gta gat cat tta ctt ctt gca ttt tta gaa gaa aga caa cat 864
Gln Thr Val Asp His Leu Leu Leu Ala Phe Leu Glu Glu Arg Gln His
275 280 285

45 ctt ttt att gta ctt gat gag tat ggg gga tta tct ggt gtt gtt tcc 912
Leu Phe Ile Val Leu Asp Glu Tyr Gly Gly Leu Ser Gly Val Val Ser

F0010150-110904

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290 295 300

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 5 305 310 315 320

agt gat aca aca cct gat ctt aga gca ctt gca aaa aaa aga cat agt 1008
 Ser Asp Thr Thr Pro Asp Leu Arg Ala Leu Ala Lys Lys Arg His Ser
 325 330 335

10 gca tta atc caa aat aat aaa aat act ctt tta aaa taa 1047
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Ile Glu His Leu Arg Glu Gln Gly Ser Lys Lys Gly Glu Lys Leu Tyr
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30 Tyr Leu His Ser Asn Ile Asp Gln Pro Ile Thr Ala Val Leu Ile Leu
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35 Asn Thr Ile Ala Asn Thr Ala Gly Ala Ala Leu Ala Gly Ala Ile Ala
 65 70 75 80

Thr Thr Thr Leu His Glu Ser Thr Lys Pro Phe Phe Ala Ala Ile Leu
 85 90 95

40 Thr Leu Leu Ile Leu Ala Phe Gly Glu Ile Ile Pro Lys Thr Leu Gly
 100 105 110

Val Ala Tyr Ser Lys Arg Ile Ala Ile Ile Leu Leu Asn Pro Leu Ser
 115 120 125

45 Ile Leu Ile Val Thr Leu Lys Pro Leu Ile Met Leu Ser Ser Tyr Leu

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130 135 140

Thr Arg Leu Val Ser Pro Arg Lys Arg Pro Thr Val Thr Glu Asp Asp
145 150 155 160

5 Ile Arg Ala Leu Thr Ser Leu Ser Arg Glu Ser Gly Arg Ile Lys Pro
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Tyr Glu Glu His Val Ile Lys Asn Ile Leu Ser Leu Asp Leu Lys Tyr
10 180 185 190

Ala His Glu Ile Met Thr Pro Arg Thr Met Val Phe Ser Leu His Glu
195 200 205

15 Asn Leu Thr Val Ser Glu Ala Tyr Ser Asn Pro Lys Ile Trp Asn Tyr
210 215 220

Ser Arg Ile Pro Thr Tyr Gly Glu Asn Asn Glu Asp Ile Thr Gly Ile
20 225 230 235 240

Ile Gln Arg Tyr Glu Ile Gly Arg Tyr Met Thr Asn Gly Glu Thr Glu
245 250 255

Lys Lys Leu Leu Glu Ile Met Gln Pro Ala Lys Phe Val Leu Glu Ser
25 260 265 270

Gln Thr Val Asp His Leu Leu Leu Ala Phe Leu Glu Glu Arg Gln His
275 280 285

30 Leu Phe Ile Val Leu Asp Glu Tyr Gly Gly Leu Ser Gly Val Val Ser
290 295 300

Leu Glu Asp Val Leu Glu Thr Met Leu Gly Arg Glu Ile Val Asp Glu
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35 Ser Asp Thr Thr Pro Asp Leu Arg Ala Leu Ala Lys Lys Arg His Ser
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F0030450-110901

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1 5 10 15

10

ata aca gaa aat tat ctc ttt gct aca tca att acc act tcc aca att 96
Ile Thr Glu Asn Tyr Leu Phe Ala Thr Ser Ile Thr Thr Ser Thr Ile
20 25 30

15

aac caa caa cat ata gca tat aca gtt act ttt acc tct cca gaa aat 144
Asn Gln Gln His Ile Ala Tyr Thr Val Thr Phe Thr Ser Pro Glu Asn
35 40 45

20

cct aat ctt gca aca gag atg gaa aca cat agt gaa tta gta aag ctt 192
Pro Asn Leu Ala Thr Glu Met Glu Thr His Ser Glu Leu Val Lys Leu
50 55 60

25

gca aat caa tct tta gat agt aaa ata ggt tta aat tta cgt gtt aaa 240
Ala Asn Gln Ser Leu Asp Ser Lys Ile Gly Leu Asn Leu Arg Val Lys
65 70 75 80

30

gaa gat ata agt aca gca caa aaa att ctt gac tcg aat ggt tat tat 288
Glu Asp Ile Ser Thr Ala Gln Lys Ile Leu Asp Ser Asn Gly Tyr Tyr
85 90 95

agt gga agt gtc gag gga aag att gac tgg cag acg aac cct att agt 336
 Ser Gly Ser Val Glu Gly Lys Ile Asp Trp Gln Thr Asn Pro Ile Ser
 100 105 110

35

atc caa atc caa ttt aaa cca aat gta caa tat aaa ata aat aca ata 384
Ile Gln Ile Gln Phe Lys Pro Asn Val Gln Tyr Lys Ile Asn Thr Ile
115 120 125

40

cat atc caa tac ctt gat agt gaa ctt gca tat ctc cct ctt tcc tta 432
His Ile Gln Tyr Leu Asp Ser Glu Leu Ala Tyr Leu Pro Leu Ser Leu
130 135 140

45

gaa gaa ttc aat ctc tct aaa ggt aat cct gct ctt gct gtt aat atc 480
Glu Glu Phe Asn Leu Ser Lys Gly Asn Pro Ala Leu Ala Val Asn Ile
145 150 155 160

- 24 -

cta tcc tct gta agt agc ctc atg caa tat ata cat aat aat gga tat 528
 Leu Ser Ser Val Ser Ser Leu Met Gln Tyr Ile His Asn Asn Gly Tyr
 165 170 175

5 cca tta gcc aaa ata aaa aaa act caa tac ata att aat cgg atg gat 576
 Pro Leu Ala Lys Ile Lys Lys Thr Gln Tyr Ile Ile Asn Arg Met Asp
 180 185 190

10 tat aca ttt gat att gat tta gta ata aga caa gga ccg tta ctc cat 624
 Tyr Thr Phe Asp Ile Asp Leu Val Ile Arg Gln Gly Pro Leu Leu His
 195 200 205

15 atg ggt aaa gta caa cct caa cat aat ctc aat att tca aca ata ttc 672
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20 cta aat aaa att gct aca tgg aag gaa gga agg gta tgg aac aat gca 720
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 225 230 235 240

ctc ctt gat tct tat cga aca cgg ctt caa caa aca ggc ctt ttc agt 768
 Leu Leu Asp Ser Tyr Arg Thr Arg Leu Gln Gln Thr Gly Leu Phe Ser
 245 250 255

25 tct ata act ctc aat cca agg aat caa aaa gaa caa aat ggt aac acc 816
 Ser Ile Thr Leu Asn Pro Arg Asn Gln Lys Glu Gln Asn Gly Asn Thr
 260 265 270

30 tct ata gaa ctt gtt gca aca gaa gcc cct cca agg act att agt ggt 864
 Ser Ile Glu Leu Val Ala Thr Glu Ala Pro Pro Arg Thr Ile Ser Gly
 275 280 285

35 ggc tta caa tac tct tct gat caa ggt att ggt gca cgt ggg act tgg 912
 Gly Leu Gln Tyr Ser Ser Asp Gln Gly Ile Gly Ala Arg Gly Thr Trp
 290 295 300

40 gaa cat cga aat gtt ttt ggt aat gga gaa ctt ttt cgt ata aca gca 960
 Glu His Arg Asn Val Phe Gly Asn Gly Glu Leu Phe Arg Ile Thr Ala
 305 310 315 320

cca ata agt cga gat gat caa aaa att atg gca aac ttc caa aaa cca 1008
 Pro Ile Ser Arg Asp Asp Gln Lys Ile Met Ala Asn Phe Gln Lys Pro
 325 330 335

45 gcc ttt ggc cgt cca aat caa tca tta att agt gaa gca caa ctt aaa 1056
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	Lys Glu Asn Thr Lys Ser Tyr Lys Gln Gln Leu Ala Ser Ile Ala Leu			
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	Gly Ile Glu Arg Gln Phe Asn Arg Arg Trp Phe Gly Ser Ser Ser Leu			
10	370	375	380	
	tca gtt gat aca gga ttt atg gat gat cga gat tct ata aaa aaa ata			1200
	Ser Val Asp Thr Gly Phe Met Asp Asp Arg Asp Ser Ile Lys Lys Ile			
	385	390	395	400
15	ttt act ctt ttt ggc atc ccc tta tca ata aca agg gat agt tct aaa			1248
	Phe Thr Leu Phe Gly Ile Pro Leu Ser Ile Thr Arg Asp Ser Ser Lys			
	405	410	415	
	gat cct ctt aat cct atc caa gga aca aaa gct acc tta aat gtt act			1296
20	Asp Pro Leu Asn Pro Ile Gln Gly Thr Lys Ala Thr Leu Asn Val Thr			
	420	425	430	
	cct tat att ggt aaa tat aaa aaa aag att ttg act tta cgt agt cgg			1344
	Pro Tyr Ile Gly Lys Tyr Lys Lys Lys Ile Leu Thr Leu Arg Ser Arg			
25	435	440	445	
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	Phe Asp Phe Ser Phe Tyr Ile Asp Val Leu Lys Thr Gly Lys Leu Ile			
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	ttg gct aac aaa ata gca ata ggt tcc ctc cta ggg aaa gat ata gaa			1440
	Leu Ala Asn Lys Ile Ala Ile Gly Ser Leu Leu Gly Lys Asp Ile Glu			
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35	aac tat cct gca ata cta agg ttt tat gct ggg ggt ggt ggt agt gta			1488
	Asn Tyr Pro Ala Ile Leu Arg Phe Tyr Ala Gly Gly Gly Gly Ser Val			
	485	490	495	
	aga ggg tat gac tat caa tca ttg gga cca aaa aat aaa tat ggg gat			1536
40	Arg Gly Tyr Asp Tyr Gln Ser Leu Gly Pro Lys Asn Lys Tyr Gly Asp			
	500	505	510	
	gct att gga gga ctt tct ttt tca act att agt ttt gaa tta cga tta			1584
	Ala Ile Gly Gly Leu Ser Phe Ser Thr Ile Ser Phe Glu Leu Arg Leu			
45	515	520	525	

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 530 535 540

5 tat tta cga aaa aaa aat ttc ctg act tta aaa aaa tca ata tat tgg 1680
 Tyr Leu Arg Lys Lys Asn Phe Leu Thr Leu Lys Lys Ser Ile Tyr Trp
 545 550 555 560

10 ggg gta ggc ctg ggg cta cga tat tat aca agt ttt gcc ccc ata cgt 1728
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 565 570 575

15 tta gat ata gca act cca ctt caa gat aga agc cat aat aaa cac ttt 1776
 Leu Asp Ile Ala Thr Pro Leu Gln Asp Arg Ser His Asn Lys His Phe
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20 caa ctt tat att agt att ggg caa gca ttc taa tga 1812
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 25 <213> Lawsonia intracellularis

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35 Asn Gln Gln His Ile Ala Tyr Thr Val Thr Phe Thr Ser Pro Glu Asn
 35 40 45

Pro Asn Leu Ala Thr Glu Met Glu Thr His Ser Glu Leu Val Lys Leu
 50 55 60

40 Ala Asn Gln Ser Leu Asp Ser Lys Ile Gly Leu Asn Leu Arg Val Lys
 65 70 75 80

Glu Asp Ile Ser Thr Ala Gln Lys Ile Leu Asp Ser Asn Gly Tyr Tyr
 85 90 95

45 Ser Gly Ser Val Glu Gly Lys Ile Asp Trp Gln Thr Asn Pro Ile Ser

F0020460-1105004

- 27 -

100 105 110

Ile Gln Ile Gln Phe Lys Pro Asn Val Gln Tyr Lys Ile Asn Thr Ile
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130 135 140

10 Glu Glu Phe Asn Leu Ser Lys Gly Asn Pro Ala Leu Ala Val Asn Ile
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Leu Ser Ser Val Ser Ser Leu Met Gln Tyr Ile His Asn Asn Gly Tyr
165 170 175

15 Pro Leu Ala Lys Ile Lys Lys Thr Gln Tyr Ile Ile Asn Arg Met Asp
180 185 190

Tyr Thr Phe Asp Ile Asp Leu Val Ile Arg Gln Gly Pro Leu Leu His
195 200 205

20 Met Gly Lys Val Gln Pro Gln His Asn Leu Asn Ile Ser Thr Ile Phe
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25 Leu Asn Lys Ile Ala Thr Trp Lys Glu Gly Arg Val Trp Asn Asn Ala
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Leu Leu Asp Ser Tyr Arg Thr Arg Leu Gln Gln Thr Gly Leu Phe Ser
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Ser Ile Glu Leu Val Ala Thr Glu Ala Pro Pro Arg Thr Ile Ser Gly
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35 Gly Leu Gln Tyr Ser Ser Asp Gln Gly Ile Gly Ala Arg Gly Thr Trp
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40 Glu His Arg Asn Val Phe Gly Asn Gly Glu Leu Phe Arg Ile Thr Ala
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Pro Ile Ser Arg Asp Asp Gln Lys Ile Met Ala Asn Phe Gln Lys Pro
325 330 335

45 Ala Phe Gly Arg Pro Asn Gln Ser Leu Ile Ser Glu Ala Gln Leu Lys
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Lys Glu Asn Thr Lys Ser Tyr Lys Gln Gln Leu Ala Ser Ile Ala Leu
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5 Gly Ile Glu Arg Gln Phe Asn Arg Arg Trp Phe Gly Ser Ser Ser Leu
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Ser Val Asp Thr Gly Phe Met Asp Asp Arg Asp Ser Ile Lys Lys Ile
 385 390 395 400

10 Phe Thr Leu Phe Gly Ile Pro Leu Ser Ile Thr Arg Asp Ser Ser Lys
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Asp Pro Leu Asn Pro Ile Gln Gly Thr Lys Ala Thr Leu Asn Val Thr
 15 420 425 430

Pro Tyr Ile Gly Lys Tyr Lys Lys Lys Ile Leu Thr Leu Arg Ser Arg
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20 Phe Asp Phe Ser Phe Tyr Ile Asp Val Leu Lys Thr Gly Lys Leu Ile
 450 455 460

Leu Ala Asn Lys Ile Ala Ile Gly Ser Leu Leu Gly Lys Asp Ile Glu
 465 470 475 480

25 Asn Tyr Pro Ala Ile Leu Arg Phe Tyr Ala Gly Gly Gly Gly Ser Val
 485 490 495

Arg Gly Tyr Asp Tyr Gln Ser Leu Gly Pro Lys Asn Lys Tyr Gly Asp
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Ala Ile Gly Gly Leu Ser Phe Ser Thr Ile Ser Phe Glu Leu Arg Leu
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35 Lys Ile Thr Glu Ser Ile Gly Ile Val Pro Ile Tyr Trp Met Gly Glu
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Tyr Leu Arg Lys Lys Asn Phe Leu Thr Leu Lys Lys Ser Ile Tyr Trp
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 Ala Phe Thr Leu Phe Leu Gly Leu Ile Ile Thr Gly Ile Leu Phe Ile
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25 cgg acc tct aca ggc att gct tgg att aaa aat aca gtt tct tct tta 144
 Arg Thr Ser Thr Gly Ile Ala Trp Ile Lys Asn Thr Val Ser Ser Leu
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ctt caa caa caa gga att ata cta caa gta tct tca att att gga cca 192
 Leu Gln Gln Gln Gly Ile Ile Leu Gln Val Ser Ser Ile Ile Gly Pro
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30 ttc cca gaa caa att act att aat gaa ctt agc ctt agt gat gtg aat 240
 Phe Pro Glu Gln Ile Thr Ile Asn Glu Leu Ser Leu Ser Asp Val Asn
 65 70 75 80

35 gga act tac ctt aca ata tct aac tta gaa atc caa tca aac tta tgg 288
 Gly Thr Tyr Leu Thr Ile Ser Asn Leu Glu Ile Gln Ser Asn Leu Trp
 85 90 95

40 gct tta ttc aaa ggt caa ctt gaa att ctg tct ttt gaa ctt aat gat 336
 Ala Leu Phe Lys Gly Gln Leu Glu Ile Leu Ser Phe Glu Leu Asn Asp
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45 ctt gta tta tat cgc tta ccc tca aat aat aat cta aaa aaa tca tct 384
 Leu Val Leu Tyr Arg Leu Pro Ser Asn Asn Asn Leu Lys Lys Ser Ser
 115 120 125

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 145 150 155 160

10 tcc tct gat att ata ggt att cca ttg gta tta tcc ctt gag ggt gat 528
 Ser Ser Asp Ile Ile Gly Ile Pro Leu Val Leu Ser Leu Glu Gly Asp
 165 170 175

15 ggt aca tta aca aat tgg aat gga aca ttt caa cta tcc tct tct aac 576
 Gly Thr Leu Thr Asn Trp Asn Gly Thr Phe Gln Leu Ser Ser Ser Asn
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 Lys Thr Lys Ile Ile Gly Thr Leu Arg Tyr Gln Gly Asn Lys Thr Gln
 195 200 205

20 ttt ttt gaa tat gtt cat cct aca cgg ata gta aca cta gag ata gac 672
 Phe Phe Glu Tyr Val His Pro Thr Arg Ile Val Thr Leu Glu Ile Asp
 210 215 220

25 agc gta gct gat aaa aag tca tat aat aat agt atc ctt gaa caa cct 720
 Ser Val Ala Asp Lys Lys Ser Tyr Asn Asn Ser Ile Leu Glu Gln Pro
 225 230 235 240

30 cta cat tta cac ctt tct att tat cct gaa cat aat aga att atc tta 768
 Leu His Leu His Leu Ser Ile Tyr Pro Glu His Asn Arg Ile Ile Leu
 245 250 255

35 cac tca tta cta gct gaa tat ggt agc tgg tta ctt aca tca gaa agt 816
 His Ser Leu Leu Ala Glu Tyr Gly Ser Trp Leu Leu Thr Ser Glu Ser
 260 265 270

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 Ile Glu Val Ser Asn Glu Gln Leu Lys Gly Asn Ile Leu Leu Lys Tyr
 275 280 285

40 aat gga gaa gct act cat caa ctt cct ata aaa aaa ctt aac tca tca 912
 Asn Gly Glu Ala Thr His Gln Leu Pro Ile Lys Lys Leu Asn Ser Ser
 290 295 300

45 att acc ctc agt ggc tca cta aat aaa cct aat ttt agt ata caa atg 960
 Ile Thr Leu Ser Gly Ser Leu Asn Lys Pro Asn Phe Ser Ile Gln Met
 305 310 315 320

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- 31 -

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	gaa ctt gtt att aat cta gga ctt ttc tct act cac tct gat att ctt	1056
	Glu Leu Val Ile Asn Leu Gly Leu Phe Ser Thr His Ser Asp Ile Leu	
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	aca tct ggg aca att aca gta cag gga gaa act ata ccc aat agt att	1104
	Thr Ser Gly Thr Ile Thr Val Gln Gly Glu Thr Ile Pro Asn Ser Ile	
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	ctt tcc agt gca gtt gat ata ata gcc tct aca aca aca cat aca att	1152
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20	Thr Leu Glu His Ala Thr Leu Thr Ser Pro Glu Met His Phe Ser Leu	
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	tct gga gaa ttt aat agt ctt cta gga aat atc gat gca aac cta aaa	1248
	Ser Gly Glu Phe Asn Ser Leu Leu Gly Asn Ile Asp Ala Asn Leu Lys	
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	ggt aat act cca act ctt agt ata ttt tct tct ctt ctt gga cta cct	1296
	Gly Asn Thr Pro Thr Leu Ser Ile Phe Ser Ser Leu Leu Gly Leu Pro	
	420 425 430	
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	Asp Leu Thr Gly Gln Ser Asn Ile Thr Ile Gly Leu His Arg Gln Gly	
	435 440 445	
	tct tcc tct tca ata gaa gga aca gca act gtc tca ctt aat aat atg	1392
35	Ser Ser Ser Ser Ile Glu Gly Thr Ala Thr Val Ser Leu Asn Asn Met	
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40	Asn Trp Gly Val Gln Ala Leu Gln Gly Thr Leu Gly Asp Asn Ala Thr	
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	cta agt gga ata tat aat tta act ccc ata gac tgg tct att tct tta	1488
	Leu Ser Gly Ile Tyr Asn Leu Thr Pro Ile Asp Trp Ser Ile Ser Leu	
	485 490 495	
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Asn Lys Leu Lys Leu Thr Ala Lys Asn Val Tyr Ala Glu Gly Leu Ile
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5 aat ttt caa aaa aaa tac ata gat agc tct ata aat ctt ata att cct 1584
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10 aac ctt cag cta ata gct cct cct ata tct gga gag tta caa tcc tta 1632
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25 ata aca ctc tcg gct gag cca gct tca tct gag gca tta acc ttt tca 1824
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 595 600 605

30 agt aat tgg gga atc cta cct acg gaa ata cta gta gaa aaa att ata 1872
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 625 630 635 640

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40 aaa gat att gca aac ata ttg caa ata cct att aga ggt tca gca tca 2016
 Lys Asp Ile Ala Asn Ile Leu Gln Ile Pro Ile Arg Gly Ser Ala Ser
 660 665 670

45 ata aaa ata cag ttt gat cca aag aat caa caa tgt att tct act caa 2064
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 675 680 685

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tgg caa tta aaa aat ttc ata tta ggt aat aat ttt aat gta act act 2112
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 690 695 700

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ata aaa gga aga gca gat aca ata caa ctt cat aag aat cct aca att 2160
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 705 710 715 720

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gct ctc tct tca aaa att ggt gct ggt aca tat gaa gac ttt caa tgg 2208
 Ala Leu Ser Ser Lys Ile Gly Ala Gly Thr Tyr Glu Asp Phe Gln Trp
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aca caa ggg acg tta gac ata aaa ggc aca tta aaa aat ttt aat agt 2256
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aaa ata aat ata gca gga caa aca act gta aac gca aac ttt caa aca 2304
 Lys Ile Asn Ile Ala Gly Gln Thr Thr Val Asn Ala Asn Phe Gln Thr
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aat ctt ttt gaa aaa aat att aat ata act act ctt aat tta aaa aat 2352
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gtc tca cct caa caa ttt gtt ctt aat aac tgt tca cta gca att ctt 2448
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aat gct aat gca atc att aaa gaa gtt tca ctt ctc tct ttc caa cca 2544
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aca gga ata cct agt aaa cct aaa gga aca ctc tca ttt gat att cta 2640

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Thr Gly Ile Pro Ser Lys Pro Lys Gly Thr Leu Ser Phe Asp Ile Leu
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5 aac ata cat tat cca agg cca aat cca tca ata gca aac tta cat gta 2688
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885 890 895

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915 920 925

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20 agg cct ttt tct gcc cat atc aag tgg act gga ata tta gat aca ctt 2880
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965 970 975

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980 985 990

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Tyr Leu Glu Asn Ile Asn Ala Lys Leu Gln Val Phe Ser Asn Arg Ile
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40 tcc cat att caa gct aca gca tct gat ggt aaa caa ggt agt ata caa 3120
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45 ctt att ggt aat att ggc tca tct aaa gaa cac ttt cct ttg tct att 3168
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ctt aca ctt tca gga gca gct act ctt gaa gga aca tta aaa cag tct 3264
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gaa gtt aaa ggc gat att gtt att aac caa ggc gaa ttt caa ctt act 3312
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aat tta cta gga aaa caa ttt tct ctt gct aaa agt aca ata tca ttt 3600
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tca gga tca gtt cca cca aac cca cta ctc aat att tct tta aca tat 3648
 Ser Gly Ser Val Pro Pro Asn Pro Leu Leu Asn Ile Ser Leu Thr Tyr
 1205 1210 1215

tca tca cct tct att aca gct ata ggc att att aaa ggt aca act agt 3696
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 1220 1225 1230

aat cct aat att act ttt tca agt aca cca cct tta cct caa gat gaa 3744

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5 ata gtt tcc caa gtt ctt ttt ggt aaa agc tca caa agt ctt agc agg 3792
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10 ata caa gcc ata caa ctt gct caa gaa tta gca aac tta aca gga ttt 3840
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15 aat act gga agt atg aat ttc cta aca aat att cga cag aca tta ggg 3888
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1380

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Arg Thr Ser Thr Gly Ile Ala Trp Ile Lys Asn Thr Val Ser Ser Leu
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10 Leu Gln Gln Gln Gly Ile Ile Leu Gln Val Ser Ser Ile Ile Gly Pro
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Phe Pro Glu Gln Ile Thr Ile Asn Glu Leu Ser Leu Ser Asp Val Asn
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15 Gly Thr Tyr Leu Thr Ile Ser Asn Leu Glu Ile Gln Ser Asn Leu Trp
85 90 95

Ala Leu Phe Lys Gly Gln Leu Glu Ile Leu Ser Phe Glu Leu Asn Asp
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25 Thr Ser Phe Val Leu Pro His Ile Ser Phe Asp Leu Thr Pro Trp Trp
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35 180 185 190

Lys Thr Lys Ile Ile Gly Thr Leu Arg Tyr Gln Gly Asn Lys Thr Gln
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Thr Gln Gly Thr Leu Asp Ile Lys Gly Thr Leu Lys Asn Phe Asn Ser
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 Asn Leu Phe Glu Lys Asn Ile Asn Ile Thr Thr Leu Asn Leu Lys Asn
 770 775 780
 10 Ile Gln Lys Asn Ile Gly Ile Lys Leu Leu Gln Pro Ile Lys Ile Ile
 785 790 795 800
 Val Ser Pro Gln Gln Phe Val Leu Asn Asn Cys Ser Leu Ala Ile Leu
 805 810 815
 15 Pro Ser Gly Thr Ile Thr Thr Asp Ile Tyr Val Thr Pro Gln Arg Leu
 820 825 830
 Asn Ala Asn Ala Ile Ile Lys Glu Val Ser Leu Leu Ser Phe Gln Pro
 20 835 840 845
 Phe Ser Ile Leu Leu Pro Gln Gly Asn Ile Asn Gly His Ile Thr Leu
 850 855 860
 25 Thr Gly Ile Pro Ser Lys Pro Lys Gly Thr Leu Ser Phe Asp Ile Leu
 865 870 875 880
 Asn Ile His Tyr Pro Arg Pro Asn Pro Ser Ile Ala Asn Leu His Val
 885 890 895
 30 Glu Gly Glu Ile Ile Ser Ser Pro Asn Asn Ile Cys Lys Leu Asn Ala
 900 905 910
 Thr Leu Thr Glu Lys Lys Glu Pro Ile Pro Ile Ser Ile Gln Ala Thr
 35 915 920 925
 Leu Pro Phe Glu Phe Thr Glu Asn Asn Ile Pro Met Leu Ser Lys Met
 930 935 940
 40 Arg Pro Phe Ser Ala His Ile Lys Trp Thr Gly Ile Leu Asp Thr Leu
 945 950 955 960
 Trp Lys Leu Ile Pro Leu Thr Asp Tyr Ile Met Ala Gly Asn Gly Ser
 965 970 975
 45 Leu Asp Ala Ser Leu Ser Gly Thr Leu Asp Ser Pro Thr Tyr Ala Ile

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980 985 990
 Ile Thr Thr Leu Ser Asn Ala Asn Phe Gln Asp Leu Ser Leu Gly Leu
 995 1000 1005
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 Tyr Leu Glu Asn Ile Asn Ala Lys Leu Gln Val Phe Ser Asn Arg Ile
 1010 1015 1020
 Ser His Ile Gln Ala Thr Ala Ser Asp Gly Lys Gln Gly Ser Ile Gln
 10 1025 1030 1035 1040
 Leu Ile Gly Asn Ile Gly Ser Ser Lys Glu His Phe Pro Leu Ser Ile
 1045 1050 1055
 15 Asn Gly Ser Phe Thr Asn Leu Ala Pro Leu Gln Arg Lys Asp Leu Ser
 1060 1065 1070
 Leu Thr Leu Ser Gly Ala Ala Thr Leu Glu Gly Thr Leu Lys Gln Ser
 1075 1080 1085
 20 Glu Val Lys Gly Asp Ile Val Ile Asn Gln Gly Glu Phe Gln Leu Thr
 1090 1095 1100
 Glu Gly Leu Thr Ser Asn Ile Pro Thr Leu Asn Val Val Asp Ser Thr
 25 1105 1110 1115 1120
 Gln Gln Gln Asn Thr Lys Thr Lys Lys Ala Thr Tyr Gln Gln Pro Thr
 1125 1130 1135
 30 Leu Ser Ile Ala Leu Ser Ile Pro Asn Arg Phe Phe Val Arg Ser Ser
 1140 1145 1150
 Met Phe Glu Ser Glu Trp Gly Gly Asn Leu Thr Ile Asn Lys Val Ile
 1155 1160 1165
 35 Thr Ser Pro Val Ile Thr Gly Ala Leu Thr Ser Ile Arg Gly Asn Phe
 1170 1175 1180
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 40 1185 1190 1195 1200
 Ser Gly Ser Val Pro Pro Asn Pro Leu Leu Asn Ile Ser Leu Thr Tyr
 1205 1210 1215
 45 Ser Ser Pro Ser Ile Thr Ala Ile Gly Ile Ile Lys Gly Thr Thr Ser
 1220 1225 1230

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Asn Pro Asn Ile Thr Phe Ser Ser Thr Pro Pro Leu Pro Gln Asp Glu
 1235 1240 1245

5 Ile Val Ser Gln Val Leu Phe Gly Lys Ser Ser Gln Ser Leu Ser Arg
 1250 1255 1260

Ile Gln Ala Ile Gln Leu Ala Gln Glu Leu Ala Asn Leu Thr Gly Phe
 1265 1270 1275 1280

10 Asn Thr Gly Ser Met Asn Phe Leu Thr Asn Ile Arg Gln Thr Leu Gly
 1285 1290 1295

Leu Asp Ile Leu Ser Leu Gly Thr Thr Ser Asn Arg Lys Ala Asn Thr
 15 1300 1305 1310

Ser Asn Ser Asn Asp Gln Ile Glu Asp Ile Pro Val Ile Glu Leu Gly
 1315 1320 1325

20 Lys Tyr Ile Thr Asp Thr Val Tyr Val Gly Val Glu Gln Ser Tyr Leu
 1330 1335 1340

Asp Ser Asn Asp Thr Gly Ala Arg Ile Ser Val Glu Leu Ala Pro Asn
 1345 1350 1355 1360

25 Phe Asn Leu Glu Gly Arg Thr Gly Thr Gln Tyr Ser Glu Ile Gly Ile
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Asn Trp Lys Lys Asp Tyr
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40 <400> 19
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Oligonucleotide probe/primer

21

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Oligonucleotide probe/primer

22

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Oligonucleotide probe/primer

23

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Oligonucleotide probe/primer

<400> 23

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gacctaagtc ttacactttc agg

23

<210> 24

5 <211> 24

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24

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<210> 25

<211> 21

<212> DNA

20 <213> Artificial Sequence

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21

30 <210> 26

<211> 22

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40 caagcaatgc ctgtagaggt cc

22

<210> 27

<211> 24

45 <212> DNA

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<220>
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10 <210> 28
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 20 ttggggaatc ctacctacg 19

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35 <210> 30
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40 <220>
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45 <400> 30
 gcaggacaaa caactgtaaa cg 22

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5 <210> 31
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15 <210> 32
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30 <210> 33
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40 <400> 33
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<220>

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<400> 34

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20

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Oligonucleotide probe/primer

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<400> 36

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T0030150-110901

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5 <210> 38
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30 <210> 40
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40 <210> 41
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<223> Description of Artificial Sequence:
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10 <212> DNA

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<210> 44

35 <211> 45

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40040460-40004

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5 <210> 45
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25 <210> 47
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30 <220>
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<210> 48
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45 <400> 48
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10040160-10001

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<210> 49
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15 <212> DNA
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<210> 51
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35 <210> 52
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45 <210> 53

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<211> 32

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5 <220>

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32

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<210> 54

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20

<210> 55

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25

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<210> 56

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<223> Description of Artificial Sequence: oligo

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<210> 57

<211> 20

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<212> DNA
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10 <210> 58
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20 <210> 59
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<212> DNA
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25 <220>
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30 <210> 60
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<400> 60
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<220>

<223> Description of Artificial Sequence: Peptide

5 <400> 61

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1

5

10

15

Met

10

<210> 62

<211> 7

15 <212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Peptide

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Ala Thr Ser Ile Thr Thr Ser

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5

25

<210> 63

<211> 45

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<223> Description of Artificial Sequence: Peptide

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35 Met His His His His His His Ser Ser Gly Leu Val Pro Arg Gly Ser

1

5

10

15

Gly Met Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp

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Ser Pro Asp Leu Gly Thr Asp Asp Asp Asp Lys Ala Met

35

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45

45 <210> 64

<211> 50

10010160-110901

- 55 -

<212> PRT

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1

5

10

15

10

Gly Met Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp

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Ser Pro Asp Leu Gly Thr Asp Asp Asp Asp Lys Ala Met Ala Asp Ile

15

35

40

45

Gly Ser

50

20

<210> 65

<211> 7

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Peptide

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30 Glu Phe Asn Leu Ser Lys Gly

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5

<210> 66

35 <211> 17

<212> PRT

<213> Artificial Sequence

<220>

40 <223> Description of Artificial Sequence: Peptide

<400> 66

Met Gly Ser Gly Ser Gly Asp Asp Asp Asp Lys Leu Ala Leu Gly His

1

5

10

15

45

Met

10010150-110001

10 <220> Description of Artificial Sequence: Peptide

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<210>	68
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        1                5                10                15

    His His His His His
30                20

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